

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Reissue Application of:

CRAIG A. SMITH et al

Appln. No.: 09/144,502

Group Art Unit: 1646

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For: DNA ENCODING TUMOR NECROSIS  
FACTOR- $\alpha$  AND - $\beta$  RECEPTORS

PROPOSED DRAWING CORRECTIONS

Assistant Commissioner  
for Patents  
Washington, D.C. 20231

Sir:

In response to the teleconference on May 27, 1999, wherein the Examiner requested that Applicants provide proposed drawings corrections, Applicants submit herewith 5 sheets of proposed drawing corrections, wherein it is proposed that Figures 2A-2B and 3A-3C be deleted in their entirety (see the Preliminary Amendment filed October 9, 1998, wherein Figures 2A-2B and 3A-3C were deleted and replaced by the Sequence Listing).

Applicants respectfully request that the Examiner approve the proposed corrections.

The Examiner is invited to contact the undersigned at his Washington telephone number on any questions which might arise.

Respectfully submitted,

  
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Figure 2A

GCGAGGCAGGCAGCCTGGAGAGAAGGCG																				28
CTGGGCTGCGAGGGCGCGAGGGCGCGAGGGCAGGGGGCAACCGGACCCCGCCCGCATCC																				87
ATG	GCG	CCC	GTC	GCC	GTC	TGG	GCC	GCG	CTG	GCC	GTC	GGA	CTG	GAG						132
Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu						-8
CTC	TGG	GCT	GCG	GCG	CAC	GCC	TTG	CCC	GCC	CAG	GTG	GCA	TTT	ACA						177
Leu	Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr						8
CCC	TAC	GCC	CCG	GAG	CCC	GGG	AGC	ACA	TGC	CGG	CTC	AGA	GAA	TAC						222
Pro	Tyr	Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr						23
TAT	GAC	CAG	ACA	GCT	CAG	ATG	TGC	TGC	AGC	AAA	TGC	TCG	CCG	GGC						267
Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly						38
CAA	CAT	GCA	AAA	GTC	TTC	TGT	ACC	AAG	ACC	TCG	GAC	ACC	GTG	TGT						312
Gln	His	Ala	Lys	Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys						53
GAC	TCC	TGT	GAG	GAC	AGC	ACA	TAC	ACC	CAG	CTC	TGG	AAC	TGG	GTT						357
Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val						68
CCC	GAG	TGC	TTG	AGC	TGT	GGC	TCC	CGC	TGT	AGC	TCT	GAC	CAG	GTG						402
Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val						83
GAA	ACT	CAA	GCC	TGC	ACT	CGG	GAA	CAG	AAC	CGC	ATC	TGC	ACC	TGC						447
Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys						98
AGG	CCC	GGC	TGG	TAC	TGC	GCG	CTG	AGC	AAG	CAG	GAG	GGG	TGC	CGG						492
Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg						113
CTG	TGC	GCG	CCG	CTG	CGC	AAG	TGC	CGC	CCG	GGC	TTC	GGC	GTG	GCC						537
Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala						129
AGA	CCA	GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC						582
Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala						143
CCG	GGG	ACG	TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG						627
Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg						158
CCC	CAC	CAG	ATC	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC						672
Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser						173
ATG	GAT	GCA	GTC	TGC	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC						717
Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala						188
CCA	GGG	GCA	GTA	CAC	TTA	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA						762
Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln						203
CAC	ACG	CAG	CCA	ACT	CCA	GAA	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC						807
His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser						218
TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	CCC	CCA	GCT	GAA	GGG	AGC	ACT						852
Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr						233
GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	ATT	GTG	GGT	GTG	ACA	GCC						897
Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala						248
TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	TGT	GTC	ATC	ATG	ACC						942
Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr						263

Figure 2B

CAG GTG AAA AAG AAG CCC TTG TGC CTG CAG AGA GAA GCC AAG GTG	987
Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val	278
CCT CAC TTG CCT GCC GAT AAG GCC CGG GGT ACA CAG GGC CCC GAG	1032
Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu	293
CAG CAG CAC CTG CTG ATC ACA GCG CCG AGC TCC AGC AGC AGC TCC	1077
Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser	308
CTG GAG AGC TCG GCC AGT GCG TTG GAC AGA AGG GCG CCC ACT CGG	1122
Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg	323
AAC CAG CCA CAG GCA CCA GGC GTG GAG GCC AGT GGG GCC GGG GAG	1167
Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu	338
GCC CGG GCC AGC ACC GGG AGC TCA GAT TCT TCC CCT GGT GGC CAT	1212
Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His	353
GGG ACC CAG GTC AAT GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC	1257
Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser	368
TCT GAC CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG	1302
Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met	383
GGA GAC ACA GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG	1347
Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln	398
GTC CCC TTC TCC AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG	1392
Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu	413
ACG CCA GAG ACC CTG CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC	1437
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro	428
CTT GGA GTG CCT GAT GCT GGG ATG AAG CCC AGT	1470
Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser	439
TAACCAGGCCGGTGTGGGCTGTGTCTGTAGCCAAGGTGGGCTGAGCCCTGGCAGGATGAC	
CCTGCGAAGGGGCCCTGGTCCTTCCAGGCCCCCACCCTAGGACTCTGAGGCTCTTTCT	
GGGCCAAGTTCCTCTAGTGCCCTCCACAGCCGAGCCTCCCTCTGACCTGCAG...	

Figure 3A

CGCAGCTGAGGCACTAGAGCTCC																	23	
AGGCACAAGGGCGGGAGCCACCGCTGCCCT																	75	
Met Ala Pro Ala Ala Leu Trp																	-16	
GTC GCG CTG GTC TTC GAA CTG CAG CTG TGG GCC ACC GGG CAC ACA																		120
Val Ala Leu Val Phe Glu Leu Gln Leu Trp Ala Thr Gly His Thr																	-1	
GTG CCC GGC CAG GTT GTC TTG ACA CCC TAC AAA CCG GAA CCT GGG																		165
Val Pro Ala Gln Val Val Leu Thr Pro Tyr Lys Pro Glu Pro Gly																	15	
TAC GAG TGC CAG ATC TCA CAG GAA TAC TAT GAC AGG AAG GCT CAG																		210
Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp Arg Lys Ala Gln																	30	
ATG TGC TGT GCT AAG TGT CCT CCT GGC CAA TAT GTG AAA CAT TTC																		255
Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val Lys His Phe																	45	
TGC AAC AAG ACC TCG GAC ACC GTG TGT GCG GAC TGT GAG GCA AGC																		300
Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu Ala Ser																	60	
ATG TAT ACC CAG GTC TGG AAC CAG TTT CGT ACA TGT TTG AGC TGC																		345
Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser Cys																	75	
AGT TCT TCC TGT ACC ACT GAC CAG GTG GAG ATC CGC GCC TGC ACT																		390
Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr																	90	
AAA CAG CAG AAC CGA GTG TGT GCT TGC GAA GCT GGC AGG TAC TgC																		435
Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys																	105	
GCC TTG AAA ACC CAT TCT GGC AGC TGT CGA CAG TGC ATG AGG CTG																		480
Ala Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu																	120	
AGC AAG TGC GGC CCT GGC TTC GGA GTG GCC AGT TCA AGA GCC CCA																		525
Ser Lys Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro																	135	
AAT GGA AAT GTG CTA TGC AAG GCC TGT GCC CCA GGG ACG TTC TCT																		570
Asn Gly Asn Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser																	150	
GAC ACC ACA TCA TCC ACT GAT GTG TGC AGG CCC CAC CGC ATC TGT																		615
Asp Thr Thr Ser Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys																	165	
AGC ATC CTG GCT ATT CCC GGA AAT GCA AGC ACA GAT GCA GTC TGT																		660
Ser Ile Leu Ala Ile Pro Gly Asn Ala Ser Thr Asp Ala Val Cys																	180	
GCG CCC GAG TCC CCA ACT CTA AGT GCC ATC CCA AGG ACA CTC TAC																		705
Ala Pro Glu Ser Pro Thr Leu Ser Ala Ile Pro Arg Thr Leu Tyr																	195	
GTA TCT CAG CCA GAG CCC ACA AGA TCC CAA CCC CTG GAT CAA GAG																		750
Val Ser Gln Pro Glu Pro Thr Arg Ser Gln Pro Leu Asp Gln Glu																	210	
CCA GGG CCC AGC CAA ACT CCA AGC ATC CTT ACA TCG TTG GGT TCA																		795
Pro Gly Pro Ser Gln Thr Pro Ser Ile Leu Thr Ser Leu Gly Ser																	225	
ACC CCC ATT ATT GAA CAA AGT ACC AAG GGT GGC ATC TCT CTT CCA																		840
Thr Pro Ile Ile Glu Gln Ser Thr Lys Gly Gly Ile Ser Leu Pro																	240	
ATT GGT CTG ATT GTT GGA GTG ACA TCA CTG GGT CTG CTG ATG TTA																		885
Ile Gly Leu Ile Val Gly Val Thr Ser Leu Gly Leu Leu Met Leu																	255	

Figure 3B

GGA CTG GTG AAC TGC ATC ATC CTG GTG CAG AGG AAA AAG AAG CCC	930
Gly Leu Val Asn Cys Ile Ile Leu Val Gln Arg Lys Lys Lys Pro	270
TCC TGC CTA CAA AGA GAT GCC AAG GTG CCT CAT GTG CCT GAT GAG	975
Ser Cys Leu Gln Arg Asp Ala Lys Val Pro His Val Pro Asp Glu	285
AAA TCC CAG GAT GCA GTA GGC CTT GAG CAG CAG CAC CTG TTG ACC	1020
Lys Ser Gln Asp Ala Val Gly Leu Glu Gln Gln His Leu Leu Thr	300
AC GCA CCC AGT TCC AGC AGC AGC TCC CTA GAG AGC TCA GCC AGC	1065
Thr Ala Pro Ser Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser	315
GCT GGG GAC CGA AGG GCG CCC CCT GGG GGC CAT CCC CAA GCA AGA	1110
Ala Gly Asp Arg Arg Ala Pro Pro Gly Gly His Pro Gln Ala Arg	330
GTC ATG GCG GAG GCC CAA GGG TTT CAG GAG GCC CGT GCC AGC TCC	1155
Val Met Ala Glu Ala Gln Gly Phe Gln Glu Ala Arg Ala Ser Ser	345
AGG ATT TCA GAT TCT TCC CAC GGA AGC CAC GGG ACC CAC GTC AAC	1200
Arg Ile Ser Asp Ser Ser His Gly Ser His Gly Thr His Val Asn	360
GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC TCT GAC CAC AGT TCT	1245
Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser	375
CAG TGC TCT TCC CAA GCC AGC GCC ACA GTG GGA GAC CCA GAT GCC	1290
Gln Cys Ser Ser Gln Ala Ser Ala Thr Val Gly Asp Pro Asp Ala	390
AAG CCC TCA GCG TCC CCA AAG GAT GAG CAG GTC CCC TTC TCT CAG	1335
Lys Pro Ser Ala Ser Pro Lys Asp Glu Gln Val Pro Phe Ser Gln	405
GAG GAG TGT CCG TCT CAG TCC CCG TGT GAG ACT ACA GAG ACA CTG	1380
Glu Glu Cys Pro Ser Gln Ser Pro Cys Glu Thr Thr Glu Thr Leu	420
CAG AGC CAT GAG AAG CCC TTG CCC CTT GGT GTG CCG GAT ATG GGC	1425
Gln Ser His Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Met Gly	435
ATG AAG CCC AGC CAA GCT GGC TGG TTT GAT CAG ATT GCA GTC AAA	1470
Met Lys Pro Ser Gln Ala Gly Trp Phe Asp Gln Ile Ala Val Lys	450
GTG GCC	1476
Val Ala	452
TGACCCCTGACAGGGGTAACACCCCTGCAAAGGGACCCCGAGACCCTGAACCCATGGAAC	1536
TTTCATGACTTTTGGCTGGATCCATTTCCCTTAGTGGCTTCCAGAGCCCCAGTTGCAGGTCA	1596
AGTGAGGGCTGAGACAGCTAGAGTGGTCAAAACTGCCATGGTGTATTTATGGGGGCGATC	1656
CCAGGAAGTTGTTGCTCTTCCATGACCCCTCTGGATCTCCTGGGCTCTTGCCTGATTCTT	1716
GCTTCTGAGAGGCCCCAGTATTTTTCCTTCTAAGGAGCTAACATCCTCTTCCATGAATA	1776
GCACAGCTCTTCAGCCTGAATGCTGACACTGCAGGGCGGTTCCAGCAAGTAGGAGCAAGT	1836
GGTGGCCTGGTAGGGCACAGAGGCCCTTCAGGTTAGTGCTAAACTCTTAGGAAGTACCCT	1896
CTCCAAGCCCACCGAAATCTTTTGATGCAAGAATCAGAGGCCCATCAGGCAGAGTTGC	1956
TCTGTTATAGGATGGTAGGGCTGTAACCTCagTGGTCCagTGTGCTTTTAGCATGCCCTGG	2016
GTTTGATCCTCAGCAACACATGCAAAACGTAAGTAGACAGCAGACAGCAGCAGCAGC	2076
CAGCCCCCTGTGTGGTTTGAGCCTCTGCCTTTGACTTTTACTCTGGTGGGCACACAGAG	2136
GGCTGGAGCTCCTCCTGACCTTCTAATGAGCCCTTCCAAGGCCACGCCCTTCTTCAG	2196
GGAATCTCAGGGACTGTAGAGTTCCAGGCCCTTCAGCCACCTGTCTCTTCTACCTCA	2256
GCCTGGAGCACTCCCTCTAACTCCCCAACGCTTGGTACTGTACTTGTGTGACCCCAAC	2316
GTGCATTGTCCGGGTTAGGCACTGTGAGTTGGAACAGCTCATGACATCGGTTGAAAGGCC	2376
CACCCGGAACAGCTAAGCCAGCTCTTTGCCAAAGGATTCATGCCGGTTTTCTAATCA	2436
CCTGCTCCCTAGCATTGCCTGGAAGGAAAGGTTTCAGGAGACTCCTCAAGAAGCAAGTTC	2496
AGTCTCAGGTGCTTGGATGCCATGCTCACCGATTCCACTGGATATGAACCTGGCAGAGGA	2556

Figure 3C

GCCTAGTTGTTGCCATGGAGACTTAAAGAGCTCAGCACTCTGGAATCAAGATACTGGACA	2616
CTTGGGGCCGACTTGTAAAGGCTCTGCAGCATCAGACTGTAGAGGGGAAGGAACACGTCT	2676
GCCCCCTGGTGGCCCGTCTGGGAtGACCTCGGGCCtCCTAGGCAACAAAAGAATGAATT	2736
GGAAAGGATGTTTCCTGGGTGTGGCCTAGCTCCTGTGCTTGTGTGGATCCCTAAAGGGTGT	2796
GCTAAGGAGCAATTGCACTGTGTGCTGGACAGAATTCCTGCTTATAAATGCTTTTTGTG	2856
TTGTTTTGTACTGAGCCCTGGCTGAGCCACCCCAACCCACCTCCCATCCCACCTTTAC	2916
ACGCCACTCTTGCAIGAGAACCTGGCTGTCTCCCACTTGTAGCCTGTGGATGCTGAGGAA	2976
ACACCCAGCCAAGTAGACTCCAGGCTTgCCCCtATCTCCTGcTaTGAGTcTggCCTCCTC	3036
AtTgTGTGTGGGAAGGAGACGGGtTCTGTcATCTCGGAAcgCCCACACCGTGGATGTGA	3096
ACAaTGGCTGTACTAGCTTAGACCAgCTTAGGGCTCTGCATATCACAGGAGGGGGAGCAG	3156
GGAAcAATTTGAGTGCTGACCTATAACAcaTTCCTAAAGGATCGGGCAGTCCAGAATCT	3216
CCTCCTTCAGT	3276
TGCATGTATGTGTGTGCCAGTGTGTGGAGCCCCGAGGTTGGCTTTGGGTGTGTTTGATCA	3336
CTCTCCAGTTACTGAGGCGGGCTCTCATCTGTACCCAGAGCTTGACATTTTCTAGTCTA	3396
ACTTGATTcAGGGATCTCTGTCTGCCTATGGAGgTGCTCAGGTTACAGGCAGGCTGCCAT	3456
ACCTGCCCCGACATTTACATGAATACTAGAGATCTGAATTCTGGTCCTCACACTTGTATAC	3516
CTGCATTTTATCCACTAAGACATCTCTCCAAGGGCTCCCCCTTCCTATTTAATAAGTTAG	3576
TTTGAActGGCAAGATGGCTCAGTGGGTAAAGCAGTTTGCGGACAAACCTGATGACCTG	3636
AGTTGGATCCCTGACCATAAGGTAGAAGAGACCTGATTCCCTGCAAGTTGTCCTCTGACCA	3696
CCACCCCATACATGCTTCTGCATATGTGCACACATCACATTCTTGACACACACTCACAT	3756
ACCATAAATGTAATAAATTTTTTAAATAAATTGATTTTATCTTTTAAAAAAAAAAAA	3813